

REMARKS

Amendments.

Applicants have amended the specification to insert SEQ ID NOs: for four sequences.

Sequence Listing.

Applicants have amended the sequence listing to comply with 37 CFR 1.821 – 1.825. Applicants have clarified that n=G, A, T, or C by the addition of numeric identifiers <220>, <221>, <222>, and <223> prior to sequence 1. One who is skilled in the art would recognize that “n” represents G, A, T, or C in a DNA sequence. Additional support for the use of “n” as any nucleotide can also be found in the USPTO’s PatentIn version 2.1 manual, table 10-2.

Applicants have also amended the sequence listing to insert the serial number of the patent application, 09/545,283 at numeric identifier <140>.

Applicants have also amended the sequence listing to include four additional sequences, sequences 8-11, on pages 5-8 of the Sequence Listing. Support for additional sequences 8-11 can be found in Figures 1-4, respectively, of the patent application.

The substitute copies of the Sequence Listing were also formatted in PatentIn version 3.0 rather than PatentIn version 2.1. Numeric identifier <170> reflects this change in the substituted “Sequence Listing.”

Applicants enclose herewith a substitute paper copy and a disk containing a computer readable copy of the Sequence Listing to comply with the formalities requirement.

Statement

The undersigned hereby certifies that:

- 1) The amendments, made in accordance with 37 CFR 1.825(a), included in the substituted sheets of the Sequence Listing are supported in the application, as filed. The substitute sheets of the Sequence Listing do not include new matter.
- 2) The content of the paper and computer readable copies of the Sequence Listing, submitted in accordance with 37 CFR 1.821(c) and (e), respectively, are the same.



The undersigned can be reached at 408-746-4512 if the Examiner wishes to discuss the response.
An early action on the merits is respectfully requested.

Respectfully submitted,

Dated: January 18, 2001

By:

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Version with markings to show changes made.

1. (Page 4)

C-type lectin receptor-like polypeptide (SEQ ID NO: 4) is approximately a 234-amino acid protein with a predicted molecular mass of approximately 26 kDa unglycosylated. Protein database searches with the BLAST algorithm indicate that the SEQ ID NO: 4 is homologous to mouse macrophage C-type lectin receptor, human dendritic cell immunoreceptor DCIR, human C-type lectin receptor DDB27, and mouse C-type lectin receptor. Figure 1 shows the BLASTP amino acid sequence alignment between SEQ ID NO: 4 (also identified as “C-type Lectin Receptor-like) and mouse macrophage C-type lectin, a type II transmembrane protein (“macrophage C-type lectin”) (SEQ ID NO: 8), indicating that the two sequences share 55% overall similarity and 39% identity. Figure 2 shows the BLASTP amino acid sequence alignment between SEQ ID NO: 4 (also identified as “C-type Lectin Receptor-like) and human dendritic cell immunoreceptor (“dendritic cell immunoreceptor”) (SEQ ID NO: 9), indicating that the two sequences share 49% identity and 69% overall similarity. Figure 3 shows the BLASTP amino acid sequence alignment between SEQ ID NO: 4 (also identified as “C-type Lectin Receptor-like) and human C-type lectin DDB27 (“DDB27”) (SEQ ID NO: 10), indicating that the two sequences share 49% identity and 69% overall similarity. Figure 4 shows the BLASTP amino acid sequence alignment between SEQ ID NO: 4 (also identified as “C-type Lectin Receptor-like) and mouse C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 6 (“mouse C-type”) (SEQ ID NO: 11), indicating that the two sequences share 44% identity and 62% overall similarity. The sequences of the present invention are expected to have C-type lectin receptor activity.

2. (Page 10)

Figure 1 shows the BLASTP amino acid sequence alignment between SEQ ID NO: 4 (also identified as “C-type Lectin Receptor-like) and mouse macrophage C-type lectin, a type II transmembrane protein (“macrophage C-type lectin”) (SEQ ID NO: 8), indicating that the two sequences share 55% overall similarity and 39% identity.

Figure 2 shows the BLASTP amino acid sequence alignment between SEQ ID NO: 4 (also identified as “C-type Lectin Receptor-like) and human dendritic cell immunoreceptor (“dendritic cell immunoreceptor”) (SEQ ID NO: 9), indicating that the two sequences share 49% identity and 69% overall similarity.

Figure 3 shows the BLASTP amino acid sequence alignment between SEQ ID NO: 4 (also identified as “C-type Lectin Receptor-like) and human C-type lectin DDB27 (“DDB27”) (SEQ ID NO: 10), indicating that the two sequences share 49% identity and 69% overall similarity.

Figure 4 shows the BLASTP amino acid sequence alignment between SEQ ID NO: 4 (also identified as “C-type Lectin Receptor-like) and mouse C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 6 (“mouse C-type”) (SEQ ID NO: 11), indicating that the two sequences share 44% identity and 62% overall similarity.